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(FILE 'HOME' ENTERED AT 13:47:12 ON 26 FEB 2003)

FILE 'CAPLUS' ENTERED AT 13:47:27 ON 26 FEB 2003

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L1          216 S BLAST AND CLUSTER
L2          156 S BLAST (3A) FUNCTION?
L3            1 S L2 AND SCORE
L4          157 S (BLAST OR FASTA) (3A) FUNCTION?
L5          154 S L4 NOT (BLAST (W) (PERIOD OR FUNACE OR VOL?))
L6           80 S L4 NOT (BLAST (W) (PERIOD OR FURNACE OR VOL?))
L7          127 S L4 NOT (BLAST (W) (CELL OR TRANSFORMATION OR WAVE))
L8           50 S L6 NOT (BLAST (W) (CELL OR TRANSFORMATION OR WAVE))
L9           18 S L8 AND (PEPTIDE OR POLYPEPTIDE OR PROTEIN)
L10          44 S (PROTEIN (5A) ALIGNMENT) (3A) (FUNCTION  OR IMPORTANCE)
L11           4 S L10 AND PATENT/DT
L12          40 S L10 NOT L11
```

=> d bib,abs 30-40

L12 ANSWER 30 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1999:294919 CAPLUS
DN 130:322323
TI Predicting enzyme function from sequence
AU Shah, Imran
CS George Mason Univ., Fairfax, VA, USA
SO (1999) 280 pp. Avail.: UMI, Order No. DA9913745
From: Diss. Abstr. Int., B 1999, 59(11), 5943
DT Dissertation
LA English
AB Unavailable

L12 ANSWER 31 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1999:115941 CAPLUS
DN 130:278727
TI The art of matchmaking: sequence alignment methods and their structural implications
AU Smith, Temple F.
CS BioMolecular Engineering Research Center, College of Engineering, Boston University, Boston, MA, 02215, USA
SO Structure (London) (1999), 7(1), R7-R12
CODEN: STRUE6; ISSN: 0969-2126
PB Current Biology Publications
DT Journal; General Review
LA English
AB A review, with 41 refs., on the **importance** of sequence **alignment** to **protein** structure prediction, modeling, and understanding.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 32 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1998:507772 CAPLUS
DN 129:213465
TI Sequence-function relationships of prokaryotic and eukaryotic galactosyltransferases
AU Breton, Christelle; Bettler, Emmanuel; Joziasse, David H.; Geremia, Roberto A.; Imberty, Anne
CS Centre de Recherches sur les Macromolecules Vegetales, CNRS, Grenoble, F-38041, Fr.
SO Journal of Biochemistry (Tokyo) (1998), 123(6), 1000-1009
CODEN: JOBIAO; ISSN: 0021-924X
PB Japanese Biochemical Society
DT Journal

LA English
AB Galactosyltransferases are enzymes which transfer galactose from UDP-Gal to various acceptors with either retention of the anomeric configuration to form .alpha.1,2-, .alpha.1,3-, .alpha.1,4-, and .alpha.1,6-linkages, or inversion of the anomeric configuration to form .beta.1,3-, .beta.1,4-, and .beta.1-ceramide linkages. During the last few years, several (c)DNA sequences coding for galactosyltransferases became available. We have retrieved these sequences and conducted sequence similarity studies. On the basis of both the nature of the reaction catalyzed and the protein sequence identity, these enzymes can be classified into twelve groups. Using a sensitive graphics method for protein comparison, conserved structural features were found in some of the galactosyltransferase groups and other classes of glycosyltransferases, resulting in the definition of five families. The lengths and locations of the conserved regions as well as the invariant residues are described for each family. In addn., the DxD motif that may be important for substrate recognition and/or catalysis is demonstrated to occur in all families but one.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 33 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1998:214166 CAPLUS
DN 128:317934
TI MrpB functions as the terminator for assembly of Proteus mirabilis mannose-resistant Proteus-like fimbriae
AU Li, Xin; Mobley, Harry L. T.
CS Department of Microbiology and Immunology, University of Maryland, Baltimore, MD, 21201, USA
SO Infection and Immunity (1998), 66(4), 1759-1763
CODEN: INFIBR; ISSN: 0019-9567
PB American Society for Microbiology
DT Journal
LA English
AB Insertional mutagenesis studies of mrpB, a putative pilin-encoding open reading frame of the mrp gene cluster, which encodes mannose-resistant Proteus-like (MR/P) fimbriae of Proteus mirabilis, indicate that MrpB functions as the terminator for fimbrial assembly.

L12 ANSWER 34 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1997:400244 CAPLUS
DN 127:132408
TI Evolution, folding and flexibility
AU Brew, Keith; Greene, Lesley
CS Department Biochemistry Molecular Biology, University Miami School Medicine, Miami, FL, 33101, USA
SO Protein Engineering (1997), 10(Suppl.), 44
CODEN: PRENE9; ISSN: 0269-2139
PB Oxford University Press
DT Journal
LA English
AB The conservation of folds in protein superfamilies with high levels of functional and sequence divergence, provides a basis for identifying the type of sequence information that dets. folds. Anal. of **alignments** of **proteins** that differ in **function** and structure-function relationships should reveal common elements that are required for their shared structural features, the superfamily fold. Conserved folds imply a conserved folding process, so that it is interesting to see how conserved sequence features relate to current models for protein folding and to test their roles by mutational studies.

L12 ANSWER 35 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1997:258210 CAPLUS
DN 126:313898
TI Adenylyl cyclases: structure, regulation and function in an enzyme

superfamily
AU Hanoune, Jacques; Pouille, Yves; Tzavara, Eleni; Shen, Tiansheng; Lipskaya, Larissa; Miyamoto, Norihiro; Suzuki, Yosuke; Defer, Nicole
CS INSERM, Hopital Henri Mondor, Creteil, 94010, Fr.
SO Molecular and Cellular Endocrinology (1997), 128(1,2), 179-194
CODEN: MCEND6; ISSN: 0303-7207
PB Elsevier
DT Journal; General Review
LA English
AB A review, with 113 refs., discussing the structure and regulatory properties of these enzymes, with special emphasis on tissue specificity.

L12 ANSWER 36 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1996:577944 CAPLUS
DN 125:295423
TI A hierarchy of SSB protomers in replication protein A
AU Philipova, Doranelly; Mullen, Janet R.; Maniar, Hina S.; Lu, Jian; Gu, Chunyan; Brill, Steven J.
CS Dep. of Molecular Biology and Biochemistry, Rutgers Univ., Piscataway, NJ, 08855, USA
SO Genes & Development (1996), 10(17), 2222-2233
CODEN: GEDEEP; ISSN: 0890-9369
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB Replication Protein A (RPA) is a heterotrimeric single-stranded DNA-binding protein (SSB) found in all eukaryotic cells. RPA is known to be required for many of the same reactions catalyzed by the homotetrameric SSB of bacteria, but its origin, subunit functions, and mechanism of binding remain a mystery. Here the authors show that the three subunits of yeast RPA contain a total of four domains with weak sequence similarity to the Escherichia coli SSB protomer. The authors refer to these four regions as potential ssDNA-binding domains (SBDs). The p69 subunit, which is known to bind ssDNA on its own, contains two SBDs that together confer stable binding to ssDNA. The p36 and p13 subunits each contain a single SBD that does not bind stably, but corresponds to the minimal region required for viability in yeast. Photocrosslinking of recombinant protein to ssDNA indicates that an SBD consists of .apprx.120 amino acids with two centrally located arom. residues. Mutation of these arom. residues inactivates ssDNA binding and is a lethal event in three of the four domains. Finally, the authors present evidence that the p36 subunit binds ssDNA, as part of the RPA complex, in a salt-dependent reaction similar to the wrapping of ssDNA about E. coli SSB. The results are consistent with the notion that RPA arose by duplication of an ancestral SSB gene and that tetrameric ssDNA-binding domains and higher order binding are essential features of cellular SSBs.

L12 ANSWER 37 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1996:286106 CAPLUS
DN 124:337217
TI Sequence-function correlation in G protein-coupled receptors
AU Kuipers, W.; Oliveria, L.; Paiva, A.C.M.; Rippmann, F.; Sander, C.; Vriend, G.; Ijzerman, A.P.
CS Department Medicinal Chemistry, Solvay Duphar B.V., Weesp, NL-1380 DA, Neth.
SO Membrane Protein Models, [Proceedings of a Conference], Leeds, U. K., Mar./Apr. 1994 (1996), Meeting Date 1994, 27-45. Editor(s): Findlay, John B. C. Publisher: Bios Scientific Publishers, Oxford, UK.
CODEN: 62UHA7
DT Conference
LA English
AB A method is presented for analyzing sequence patterns in a multiple protein family. Pairwise comparisons of sequence positions can be used to search for functionally important residues without any prior knowledge.

Residues can also be compared with properties of the proteins that are coded in so-called pseudo residues. These comparisons can be used to prove or disprove hypotheses, or to search for residues responsible for specific functional characteristics. For several ligand binding studies, the author's analyses led to a better understanding of the receptor models. In other cases, this correlation anal. has helped circumvent the structure in the central protein research paradigm: sequence to structure to function.

L12 ANSWER 38 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1995:386732 CAPLUS
DN 122:152577
TI Constrained multiple sequence alignment using XALIGN
AU Wishart, David S.; Boyko, Robert F.; Sykes, Brian D.
CS Department of Biochemistry, University of Alberta, Edmonton, AB, T6G 2S2, Can.
SO CABIOS, Computer Applications in the Biosciences (1994), 10(6), 687-8
CODEN: COABER; ISSN: 0266-7061
DT Journal
LA English
AB The program XALIGN (X-ray ALIGNment), a menu-driven, modular program designed to perform up to 6 different **alignment functions** is described, including: pairwise **protein** sequence alignment, multiple (>500) sequence alignment, pairwise sequence/structure alignments, multiple (>500) sequence/structure alignments, multiresidue clustering (for editing and alignment), and multiresidue anchoring (for editing and alignment). XALIGN is illustrated by the sequence alignment of 4 remotely related apolipophorins.

L12 ANSWER 39 OF 40 CAPLUS COPYRIGHT 2003 ACS
AN 1994:317218 CAPLUS
DN 120:317218
TI Bridging the gap. Joining of nonhomologous ends by DNA polymerases
AU King, Jeff S.; Fairley, Cecila F.; Morgan, William F.
CS Lab. Radiobiol. Environ. Health, Univ. California, San Francisco, CA, 94143, USA
SO Journal of Biological Chemistry (1994), 269(18), 13061-4
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB DNA double strand breaks with noncomplementary ends can be joined by mechanisms of nonhomologs recombination. In some systems a DNA end with a 3'-protruding single strand (PSS), which does not have a recessed 3'-hydroxyl that can allow for fill-in DNA synthesis, is joined to a blunt end with preservation of the 3'-PSS. It has been proposed that this process occurs via single strand ligation or is facilitated by an alignment protein. The authors were interested in testing the hypothesis that a DNA polymerase could **function** as this putative **alignment protein**. To characterize polymerase activities in this type of reaction, the authors incubated short double-stranded oligonucleotides that had an excess of one of the strands with an exonuclease-free Klenow fragment of Escherichia coli polymerase I, Taq DNA polymerase from Thermus aquaticus, or an exonuclease-free Stoffel fragment of Taq DNA polymerase. Products were analyzed by using biotinylated oligonucleotides sepd. by denaturing polyacrylamide gel electrophoresis. To further assess the effect of DNA polymerases on the joining of 3'-PPS ends to blunt ends, the authors incubated linear plasmid DNA with the polymerases and subjected the DNA to Southern blot and sequence anal. The authors detd. that these DNA polymerases can use a 3'-PPS end as a template after priming off the 3'-hydroxyl of a blunt end. This implies that the joining of noncomplementary ends in eukaryotic cells could proceed by a similar mechanism.

L12 ANSWER 40 OF 40 CAPLUS COPYRIGHT 2003 ACS

AN 1993:489321 CAPLUS
DN 119:89321
TI Sequence similarities between cell regulation factors, heat shock proteins and RNA helicases
AU Mian, I. Saira
CS Sinsheimer Lab., Univ. California, Santa Cruz, CA, 95064, USA
SO Trends in Biochemical Sciences (1993), 18(4), 125-7
CODEN: TBSCDB; ISSN: 0376-5067
DT Journal
LA English
AB Sequence **alignment** for a conserved domain in **proteins** involved in membrane **functions**, cell cycle, gene expression and heat shock is reported.